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The Biodiversity of Deadwood-associated Arthropods in the southern Appalachian Mountains

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BIODIVERSITY OF DEADWOOD-ASSOCIATED ARTHROPODS IN THE SOUTHERN APPALACHIAN MOUNTAINS

by
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ABSTRACT

ISABELLE NICOLE ONG: Biodiversity of Deadwood-associated Arthropods in the southern Appalachian Mountains (Under the direction of Dr. Ryan Garrick)

A biodiversity hotspot is a location that has significantly elevated levels of biodiversity including many species found nowhere else, and which is also in danger of losing much of this diversity. By identifying biodiverse regions, conservation efforts can be targeted to those locations where they are likely to have the most beneficial impacts. We looked at deadwood associated arthropods within the Southern Appalachian Mountains to examine centers of biodiversity. Nine logs were sampled, three of which were located in Bankhead National Forest and six were located in the Great Smoky Mountains. Polymerase chain reaction was used to amplify the mitochondrial cytochrome oxidase I (COI) 'barcoding' region of each of the sampled arthropods, and these products were then sequenced. Preliminary molecular taxonomic identification of specimens was achieved by comparing their COI sequences to those in public databases, and by using levels of similarity to assign them to species, genus, family and/or order. This information was used to calculate species richness for each log. Next, a phylogenetic tree was created and a phylogenetic diversity value was calculated for each log. There was a strong positive correlation between the two metrics, but phylogenetic diversity provided slightly more information for rank-ordering logs from highest to lowest biodiversity. Comparative analyses of species richness and phylogenetic diversity for other ecological communities should be conducted for a better understanding of their relationship. Overall, biodiversity was higher in Bankhead National Forest compared to the Great Smoky Mountains. This could be due to the varying types of management in the two regions, with past events and ongoing practices that affect the amount of deadwood being especially important. This study highlights the significance of biodiversity and the use of phylogenetic diversity as a metric for conservation efforts.

TABLE OF CONTENTS

LIST OF TABLES AND FIGURES

LIST OF ABBREVIATIONS

BLAST	basic local alignment search tool
bp	base pair
BSA	bovine serum albumin
COI	cytochrome c oxidase I
dH_2O	distilled water
DNA	deoxyribose nucleic acid
dNTPs	deoxynucleotide triphosphates
gDNA	genomic deoxyribonucleic acid
GRSM	Great Smoky Mountains
mg	milligram
mM	millimolar
mtDNA	mitochondrial DNA
NCBI	National Center for Biotechnology Information
NF	National Forest
PCR	polymerase chain reaction
TBE	Tris-borate-EDTA
U	unit
µL	microliter
µM	micromolar
V	volts

INTRODUCTION

The importance of biodiversity, and conservation of hotspots

Biodiversity is important for ecosystem functioning. Generally, it refers to the variety of life in the world or within a specified region. For example, biodiversity can include all of the plants, animals, and microorganisms in an area (EPA 2021). Species not only interact with and influence one another within the ecosystem they share, but their roles (e.g., primary producers, decomposers, herbivores predators etc.) are often overlapping in a community. Because of this, biodiversity is an important indicator of long-term persistence and resilience to environmental stress such as habitat loss, overexploitation, and other human activities. In 2008, the Food and Agriculture Organization estimated that approximately 32% of Atlantic cod fish stocks were overexploited, depleted, or recovering from depletion (FAO 2010). This is concerning since many humans depend on these fish stocks for food. By identifying regions of low biodiversity, conservation efforts can be focused on these areas. Biodiversity is important for other reasons too, including the promotion of a healthier ecosystem culturally, economically and environmentally.

A *biodiversity hotspot* is a location that has significantly elevated levels of biodiversity including many species found nowhere else, and which is also in danger of losing much of this diversity. Some definitions specify that such areas must have at least 1,500 endemic vascular plant species, and have been reduced to 30% or less of its original natural vegetation (Conservation International 2021). By identifying biodiverse regions, conservation efforts can be targeted to those locations where they are likely to have the most beneficial impacts. The North American Coastal Plain has recently been recognized as a biodiversity hotspot (Noss et al. 2015). Several studies have converged to overturn previous myths regarding the region and demonstrate the biological richness that it contains. The human population in combination with rising sea levels, places the North American Coastal Plain region at high risk (Noss et al. 2015). Conservation priorities for this newly recognized hotspot include reducing population growth and urban sprawl, identifying climatic refugia and biodiversity hotspots at a finer scale across the region, protecting these areas in new reserves, maintaining and restoring movement corridors, and restoring or mimicking natural disturbance (especially fire) and hydrological regimes (Noss et al. 2015).

The southern Appalachian Mountains: a center of endemism, near a biodiversity hotspot

The Appalachian Mountains are a great highland system that forms a natural barrier between the eastern Coastal Plain and the vast Interior Lowlands of North America. In the southern Appalachian Mountains, the peaks of North Carolina's Black Mountains and the Great Smoky Mountains rise above 1,825 meters. During the Pleistocene Epoch (about 2.6 million

years ago to 11,700 years ago), continental ice sheets flowed down over North America, covering New England but reaching no nearer the southern Appalachians than the Ohio River valley (Dykeman 2021). As the ice sheets advanced into temperate areas, many northern taxa experienced a reduction in range, while others were completely decimated. Thus, the southern Appalachians became an important refuge, and this is reflected by its current high levels of biodiversity (Figure 1). Once the ice sheets receded, recolonization of the northern region occurred rapidly. The exponential growth of founding populations and subsequent resource competition may have prevented other refugial populations from expanding simultaneously, and recently recognized regions may be characterized by low levels of diversity (Walker et. al 2009).

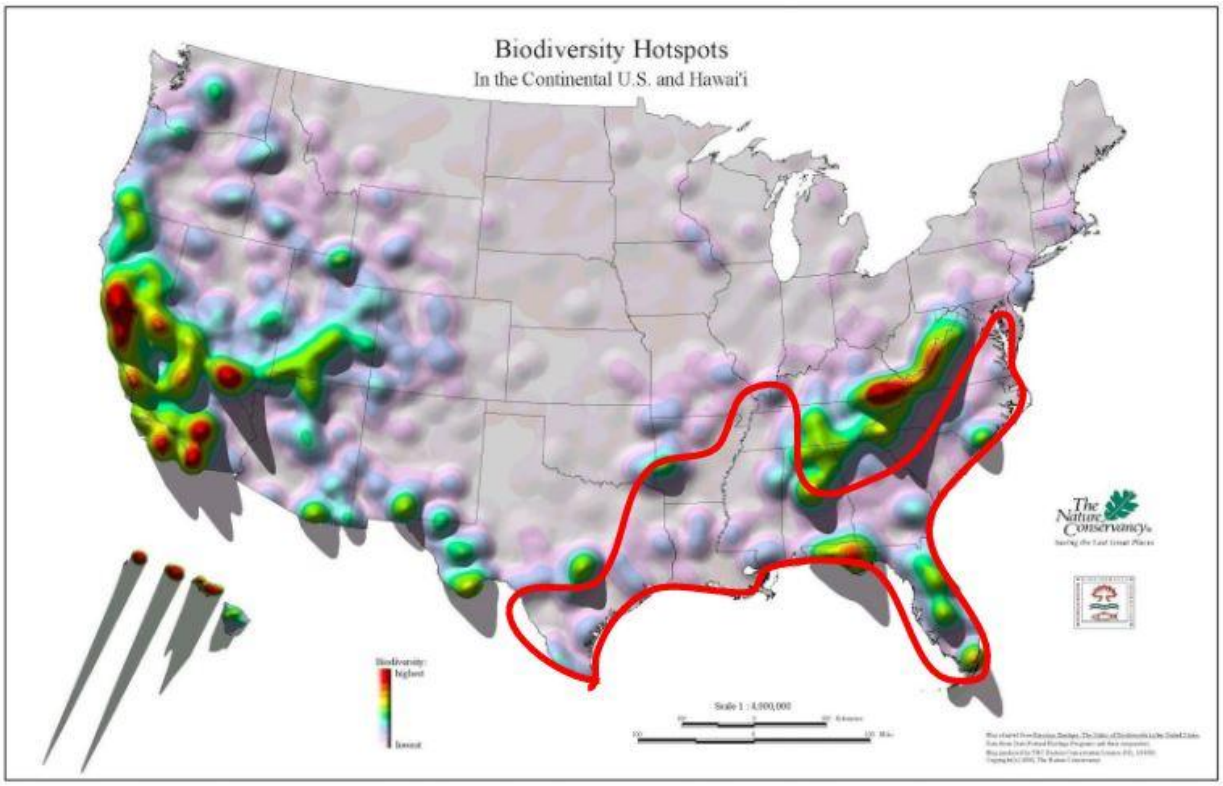

Figure 1. Map showing the geographic distribution of biodiversity in the continental U.S. and Hawaii, represented by color coding (red "hot" indicates high biodiversity, whereas "cooler" blue and grey indicate lower biodiversity). The outline in red indicates the North American Coastal Plains. Source: The Nature Conservancy (https://secpnc.files.wordpress.com/2011/08/biodiversity-hotspots-map.jpg).

The numerous glacial cycles throughout the Pleistocene have left their mark on modern populations and communities. Phylogeographical studies that focused on eastern North America often cite Pleistocene barriers to gene flow as the Appalachian Mountain discontinuity (Soltis et al. 2006). However, there is not always a clear distinction between east–west of the Appalachians; there can be integrations between the two. Nonetheless, examples of animals that commonly showed evidence for the Appalachian Mountain discontinuity include salamanders,

and turtles (Soltis et al. 2006). This general pattern typically has been attributed to survival in two distinct refugia on opposite sides of the Appalachians. Although there has been a lot of research on genetic divisions within and among lowland species in the southern Appalachians, much less research has looked at species and communities that live at mid- to high elevations, and so conservation planning does not often consider fauna restricted to habitats that occur in upland habitats (Hyseni & Garrick 2019).

The ecologically important deadwood-associated (saproxylic) arthropod community

Saproxylic organisms are those species that depend on dead or decaying wood, and they are of particular interest given their diversity. Between one fifth and one third of all forest invertebrate species are saproxylic, meaning they depend directly or indirectly on dying or dead wood (Speight 1989). These animals are known to play major roles in decomposition and nutrient cycling, making them an important part of the forest ecosystem (Hyseni & Garrick 2019). Since forest management often removes dead and decaying wood, these species are particularly vulnerable to forest management decisions. Thus, by measuring the levels of biodiversity in deadwood-associated arthropod communities in the mid- to high elevation areas of southern Appalachian Mountains (Figure 2), an understanding of how best to protect and manage the region's biodiversity can be obtained.

Figure 2. Examples of dead wood habitats in the southern Appalachian Mountains (A), and arthropod species that are associated with these habitats for some or all of their life cycle (B). Shown here are species of cockroach (*Cryptocercus punctulatus*), termite (*Reticulitermes flavipes*), beetle (*Lucanus elaphus*) and centipede (*Scolopocryptops sexspinosus*).

Approaches for measuring biodiversity, and applications to understudied communities

The traditional method of measuring biodiversity is quantifying species richness (Gotelli 2001). This simple measure counts the number of different species detected within a specified region, for a certain amount of sampling or survey effort (Gotelli 2001). However, because all species are weighted equally, this measure does not distinguish between closely vs. distantly related species. For example, a site with 10 species from the same Order would be considered to have the same level of biodiversity as a site with 10 species each from a different Order. In contrast, phylogenetic diversity looks at how closely related the species are to one another by lineage (Faith 1992). Based on a phylogeny that includes all species, phylogenetic diversity for a set of species from one location is calculated as the sum of all the lengths of the branches on the tree that span the members of the set from that site, going back to the root of the tree (Faith 1992). However, these two methods do not measure how many individuals there are per species. Other methods that include abundance exist, but here we focus only on species richness and phylogenetic diversity.

The mitochondrial DNA (mtDNA) cytochrome c oxidase I (COI) "barcoding" gene region is widely used for molecular species identification of animals (Hebert et al. 2003). There are two main advantages to using the COI gene. The first is that universal primers exist and are very robust, and the second is that the COI gene appears to show many more mutational differences among species compared to within species (Hebert et al. 2003). Aside from ease of acquisition and alignment of DNA sequences, the COI gene has the amount of variability that is sufficient to enable a reliable assignment of organisms to taxonomic categories (Hebert et al. 2003). After identifying species by their DNA, an estimate of phylogenetic relationships among taxonomic groups can be performed using the same sequences.

Goals of this study

The purpose of this study was to measure the biodiversity of deadwood-associated arthropods in the southern Appalachian Mountains using species richness and phylogenetic diversity, and to compare outcomes of the two measures. By using molecular species identification, an understanding will be gained of what types of species are present. Also, by identifying geographic regions with locally high biodiversity we can determine if there are clusters of hot and cold spots, which may be caused by the mountainous topography of the study

region. Based on the results from this work, methods of conservation can be implemented to preserve the region.

METHODS

Saproxylic arthropod specimen collections

Methods used to sample saproxylic arthropods from rotting logs in the southern Appalachians are described by Garrick et al. (2019). Briefly, two forest regions were targeted: Bankhead National Forest, Alabama (specimens collected from 3 logs across 2 sites were used in this study), and Great Smoky Mountains National Park, Tennessee and North Carolina (6 logs across 4 sites). More information regarding the logs is shown in Table 1. Arthropods at any life stage were collected from logs, preserved in 95% ethanol, and then sorted into morphotype groups. Although the present study did not involve sampling or sorting of specimens, new DNA sequence data were generated for some of these specimens (N=25) and combined with an existing data.

Table 1: Locations of nine rotting logs used in this study, and their identification (ID) code. Abbreviations are: NF, National Forest; GRSM, Great Smoky Mountains National Park; AL, Alabama; TN, Tennessee.

Log ID	Forest region	Site name	Latitude	Longitude	Elevation (m)
C01	Bankhead NF, AL	Houston Recreation Area	34.12192	-87.29025	198
C12	Bankhead NF, AL	Houston Recreation Area	34.12120	-87.29002	208
C15	Bankhead NF, AL	Corinth Recreation Area	34.10230	-87.32407	181
C25	GRSM, TN	Big Witch Gap Overlook	35.52532	-83.22337	1272
C37	GRSM, TN	Gunters Cemetery	35.77150	-83.21331	591
C39	GRSM, TN	Gunters Cemetery	35.77123	-83.21352	592
C40	GRSM, TN	Gunters Cemetery	35.77142	-83.21355	582
C44	GRSM, TN	Greenbrier	35.73249	-83.41127	466
C47	GRSM, TN	Little River Rd	35.67926	-83.55930	510

DNA extraction and genetic data generation

DNA extraction was performed using a Qiagen DNeasy Blood and Tissue kit, following the manufacturer's protocol. Depending on the size of the invertebrate, DNA was extracted either from legs only, or from whole bodies. An aliquot of the extracted DNA was then diluted (1:19) with dH_2O. The polymerase chain reaction (PCR) was used to amplify a section of the COI gene.

Each reaction was made up of a master mix containing the components shown in Table 2. The recipe makes 13.5 µL of master mix which was combined with 1.5 µL of DNA in a tube. Larger batches of master mix were made in accordance with the number of samples being amplified. When necessary, several different primer pair combinations were tested. The PCR primers used to amplify COI from all of the specimens used in this study are shown in Table 3.

Table 2: PCR master mix recipe.

Master mix component (concentration)	**Volume (µL) per reaction**
5X Buffer	3.00
$MgCl_2$ (25 mM)	1.20
dNTPs (1.25 mM)	2.40
BSA (10 mg/µL)	0.75
dH_2O	4.50
Forward primer (10 µM)	0.75
Reverse primer (10 µM)	0.75
Go-*Taq* DNA polymerase (5U/µL)	0.15

Table 3: List of forward and reverse primers.

Forward primer (5' to 3')	**Reverse primer (5' to 3')**	**Reference**
C1-J-1718: GGAGGATTTGGAAATTGATTAGTTCC	C1-N-232: ACTGTAAATATATGATGAGCTCA	Simon et al. (1994)
LCO1490: GGTCAACAAATCATAAAGATATTGG	HCO2198: TAAACTTCAGGGTGACCAAAAAATCA	Folmer et al. (1994)

After the PCR master mix plus diluted template DNA were prepared, a touch-down PCR profile (Table 4) was used to amplify the target COI gene region. A touch-down PCR profile is where the initial annealing temperature is gradually reduced after each cycle, for the first few cycles (in our case, 8 cycles). The lower annealing temperatures allow for some mismatches between primers and template DNA, which might be useful for some species. A negative control containing no genomic DNA was used to ensure there was no contamination of the master mix and to ensure that the amplified product is only the target species in your diluted genomic sample.

Table 4: PCR touchdown profile.

Steps:	Temperature	Time (mins)	Number of cycles
1	95℃	2:00	1x
2	95℃	0:30	8x
	54℃ -1℃/cycle	0:30	
	72℃	1:00	
3	95℃	0:30	30x
	50℃	0:30	
	72℃	1:00	
4	72℃	2:00	1x
5	12℃	∞	1x

Once PCR amplification was complete, agarose gel electrophoresis was used for visualization of products. Agarose gels were made of 1.5 g of agarose powder, 100 mL of 1x TBE Buffer and 1.5 µL of Gel Red. Four microliters of PCR product were pipetted into each well, and a 100-bp DNA ladder was included as a size standard. The gel was run at 100 V for 1.5 hours. A successful amplification occurred when a band was bright and easy to see with minimal streaking. Following gel electrophoresis, successfully amplified PCR products were purified using ExoSAP-IT, and then sent to Yale University for sequencing.

Data Analysis

After receiving the sequence data files from Yale, they were edited by eye for quality, trimmed and aligned, using MEGA v.7 (Kumar et al. 2016). Next, a nucleotide basic local alignment search tool (BLAST) search was performed to identify the closest matching COI sequence in the National Center for Biotechnology Information (NCBI) database for each arthropod. BLAST directly approximates alignments that optimize a measure of local similarity (Altschul et al. 1990). The following changes to the default settings were made for the NCBI nucleotide blast search: under choose search set, the database was set to “standard databases”; and under program selection, it was optimized for “somewhat similar sequences” (blastn). Sequence identity along with query cover were recorded. Identity is the sequence similarity between the query and database sequence, measured as the proportion of identical nucleotides between two sequences (e.g., if our arthropod sequence was 100% the same as database sequence, identity would be 1.0). Sequence similarity thresholds for different levels of

DNA-based taxonomic identification reported by Telfer et al. (2015) were used. These provide cut-offs for deciding whether we could confidently assign our sequence to species-level identification, or whether we could only go to genus-level, or above (Table 5). If the BLAST search returned two different matches with equal sequence identity scores, the match with the high query cover was used. After identifying each sequence to species (or genus, or family, etc.) using BLAST searches, species richness was calculated simply as the number of different species per rotting log.

Table 5: Telfer et al.'s (2015) COI sequence identity thresholds used for molecular taxonomic identification of deadwood-associated arthropods.

COI sequence identity threshold	**Taxonomic level of identification**
>0.979	Species
0.949-0.979	Genus
0.849-0.948	Family
<0.849	Order or above

MEGA was used to create a phylogenetic tree containing all COI sequences using the Neighbor-Joining algorithm (Saitou & Nei 1987), based on the uncorrected proportion of differences (*p*-distances; Nei & Kumar 2000). Closely related groupings of species were identified and a single representative of each (i.e., the one with the longest sequence) was selected for inclusion in a new input file. Once all redundant sequences were removed, a second tree was created from the new subset. This tree was used to calculate phylogenetic diversity for each of the nine rotting logs using PHD Online software (Chao & Chiu 2017) The settings for PHD Online were: data type = incidence (i.e., for each site, data consist of species detection/non-detection), and diversity order q = 0 (i.e., corresponding with Faith's phylogenetic diversity).

RESULTS

A total of 75 COI sequences were obtained from arthropods sampled from rotting logs across the Southern Appalachian region. The most successful primer pair for amplifying the COI gene was LCO1490 with HCO2198 (Folmer et al. 1994). The shortest COI sequence obtained was 452 base pairs (bp) long while the longest was 780 bp. The mean length of the COI sequence obtained was 613 bp. Based on the BLAST searches and the confidence levels using Telfer et al.'s (2015) sequence identity thresholds, 58.7% of the samples were identified to species (Figure 3). Since not all samples were identified to species taxonomic level, aliases such as "genus1 species1" were assigned. The order Blattodea had the highest percentage of

specimens identified to species level; however, other orders did not show any similarity in success.

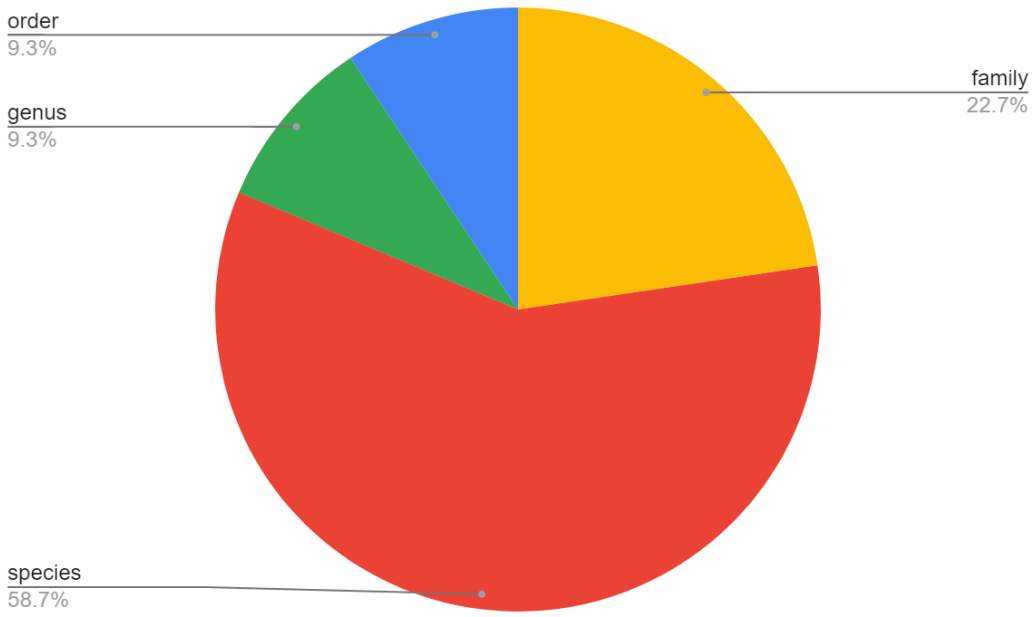

Figure 3: Resolution of molecular taxonomic identification based on BLAST searches in the NCBI database, and Telfer et al.'s (2015) COI sequence similarity thresholds.

Fourteen different arthropod orders were represented in the data set (Figure 4). The order Coleoptera (beetles) was the most well represented order. This was followed by Hymenoptera and Araneae. The order Hymenoptera contains ants, bees and wasps. However, in this study, only samples of ants were obtained. The order Araneae includes true spiders. The order Blattodea includes cockroaches and termites. In our dataset, 70% of the samples were cockroaches and 30% were termites.

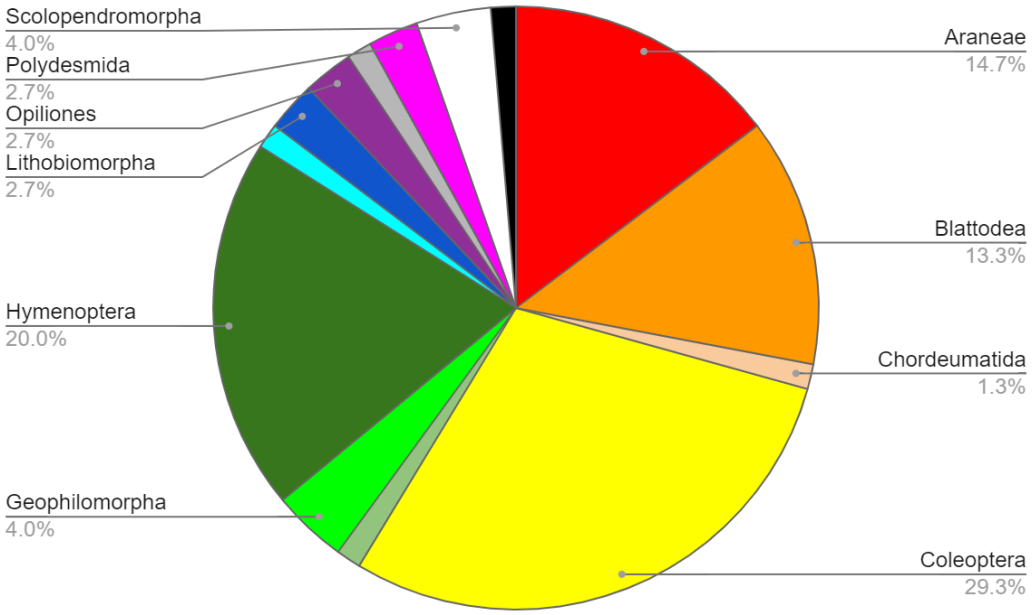

Figure 4: Proportion of different arthropod orders represented in the samples. The top 10 most well-represented orders are labeled.

The phylogenetic tree based on non-redundant sequences generally shows clustering together of members of the same order, but not always (Figure 6). The bootstrap values labeled at the nodes show confidence in the evolutionary relationship on a scale of 0 to 100, with 100 being the most confidence. The order Araneae, shown in red, is connected by a node with a 99% bootstrap value. This shows high confidence that the members of this cluster are close evolutionary relatives. Other orders that show monophyletic clustering include Hymenoptera (dark green, bootstrap support = 100), Geophilomorpha centipedes (lime green, bootstrap support = 100), Blattodea (orange, bootstrap support = 94), Opiliones (purple, bootstrap support = 100), and Lithobiomorpha centipedes (dark blue, bootstrap support = 97). The order Blattodea, shown in orange, is monophyletic but embedded within the order Coleoptera, shown in yellow. The beetles *Odontotaenius disjunctus* and Curculionidae species 1 appear to be outliers compared to the phylogenetic position of all other beetles. These specimens were sampled from the same log (C15), which also contained other arthropods in the Coleoptera order.

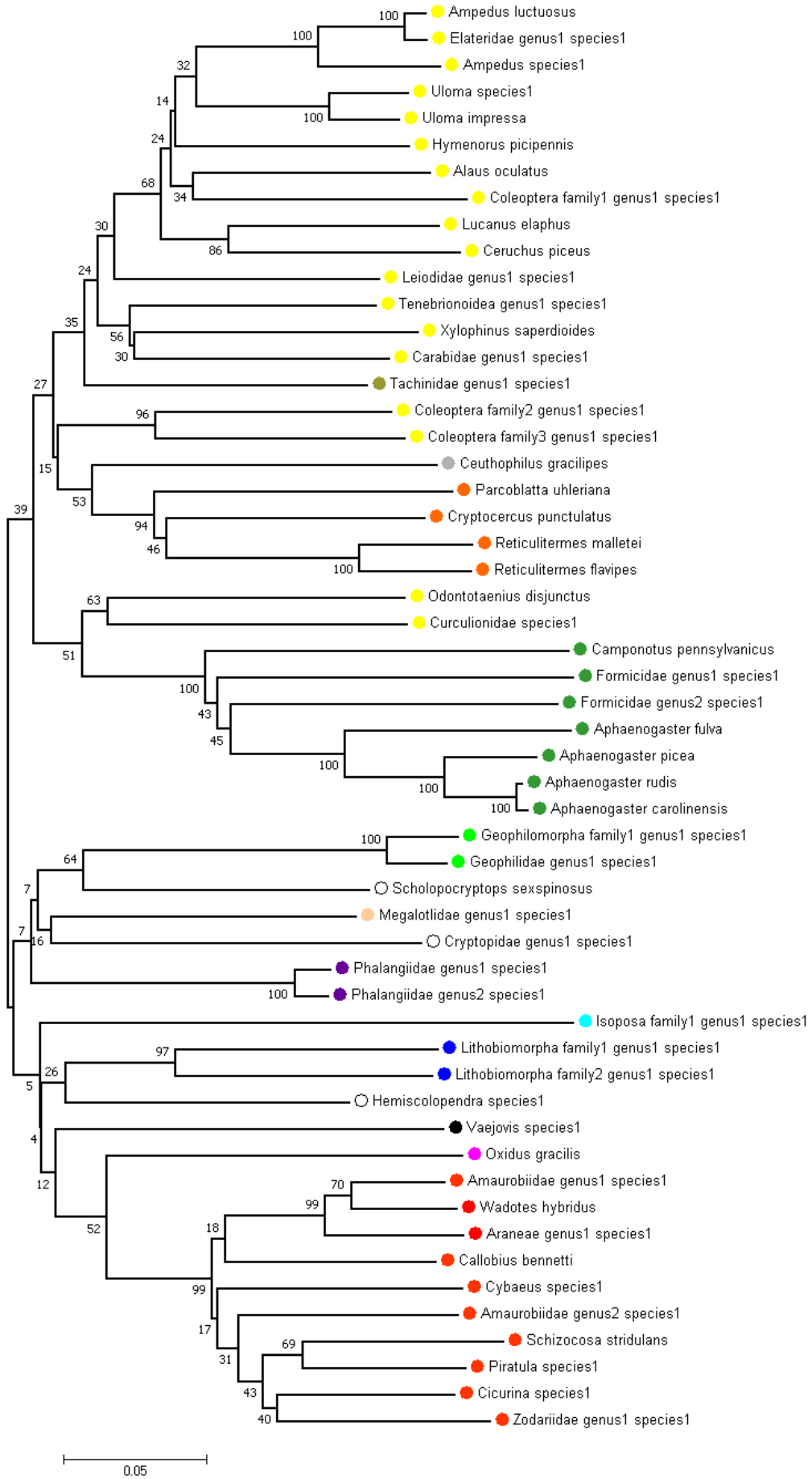
Ampedus luctuosus
Elateridae genus1 species1
Ampedus species1
Uloma species1
Uloma impressa
Hymenorus picipennis
Alaus oculatus
Coleoptera family1 genus1 species1
Lucanus elaphus
Ceruchus piceus
Leiodidae genus1 species1
Tenebrionoidea genus1 species1
Xylophinus saperdioides
Carabidae genus1 species1
Tachinidae genus1 species1
Coleoptera family2 genus1 species1
Coleoptera family3 genus1 species1
Ceuthophilus gracilipes
Parcoblatta uhleriana
Cryptocercus punctulatus
Reticulitermes malletei
Reticulitermes flavipes
Odontotaenius disjunctus
Curculionidae species1
Camponotus pennsylvanicus
Formicidae genus1 species1
Formicidae genus2 species1
Aphaenogaster fulva
Aphaenogaster picea
Aphaenogaster rudis
Aphaenogaster carolinensis
Geophilomorpha family1 genus1 species1
Geophilidae genus1 species1
Scholopocryptops sexspinosus
Megalotlidae genus1 species1
Cryptopidae genus1 species1
Phalangiidae genus1 species1
Phalangiidae genus2 species1
Isoposa family1 genus1 species1
Lithobiomorpha family1 genus1 species1
Lithobiomorpha family2 genus1 species1
Hemiscolopendra species1
Vaejovis species1
Oxidus gracilis
Amaurobiidae genus1 species1
Wadotes hybridus
Araneae genus1 species1
Callobius bennetti
Cybaeus species1
Amaurobiidae genus2 species1
Schizocosa stridulans
Piratula species1
Cicurina species1
Zodariidae genus1 species1
0.05

Figure 5: Phylogenetic tree showing relationships among representatives of each taxon (54 sequences) sampled from nine rotting logs in two study regions within the southern Appalachians. The tree was inferred using neighbor-joining. Distances were computed using p-distances and are in the units of the number of base differences per site. Color coding represents different arthropod orders, and follows Figure 4.

Species richness, shown in Table 6, was calculated as the number of different species present in each log. Although not all samples were identified by taxonomic name, sequence similarity between samples differed enough to be labeled as different species. Log C15, located in Bankhead National Forest, had the highest species richness. The average species richness per log in Bankhead National Forest was 10.33 while the average species richness per log in the Great Smoky Mountains National Park was 5.33. Phylogenetic diversity was highest for the log C15 with 1.55 which also had the highest species richness. The lowest phylogenetic diversity value was 0.27 for the log C37 which also had the lowest species richness. Graphing phylogenetic diversity versus the species richness, as shown in Figure 6, it can be seen that there is a positive correlation between the two values (R^2 value of 0.986).

Table 6: Species richness and phylogenetic diversity per log.

	Bankhead NF			Great Smoky Mountains NP					
Log ID	C01	C12	C15	C25	C37	C39	C40	C44	C47
Species richness	8	10	13	10	2	3	4	3	10
Phylogenetic diversity	1.10	1.36	1.55	1.27	0.27	0.45	0.63	0.43	1.26

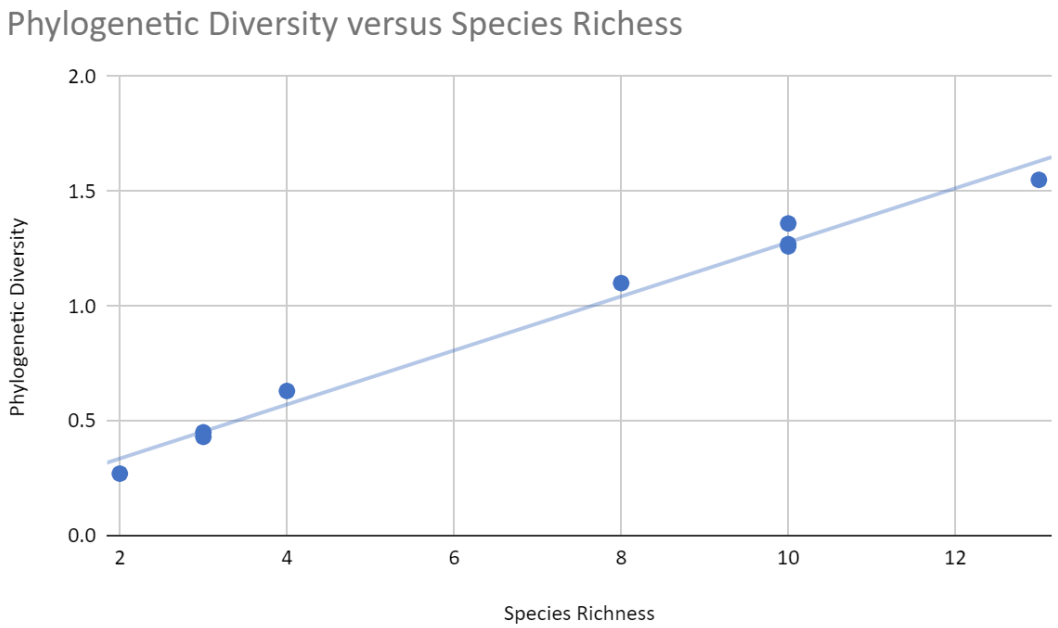

Figure 6: Phylogenetic diversity versus species richness of deadwood-associated arthropods, based on nine rotting logs from two forest regions in the southern Appalachians Mountains.

There were three logs with a species richness value of 10: log C12, C25 and C47; however, they each have slightly different phylogenetic diversity values. Log C12, located in Bankhead NF has the highest phylogenetic diversity value of 1.36 while log C25 and log C47, located in Great Smoky Mountains National Park, have similar phylogenetic diversity values, 1.27 and 1.26 respectively. Figure 7 shows a heat map of levels of biodiversity in each of the two forest regions included in this study, based on both species richness and phylogenetic diversity. There is unexpectedly high biodiversity in Bankhead National Forest located in Alabama in comparison to the Great Smoky Mountains located in Tennessee.

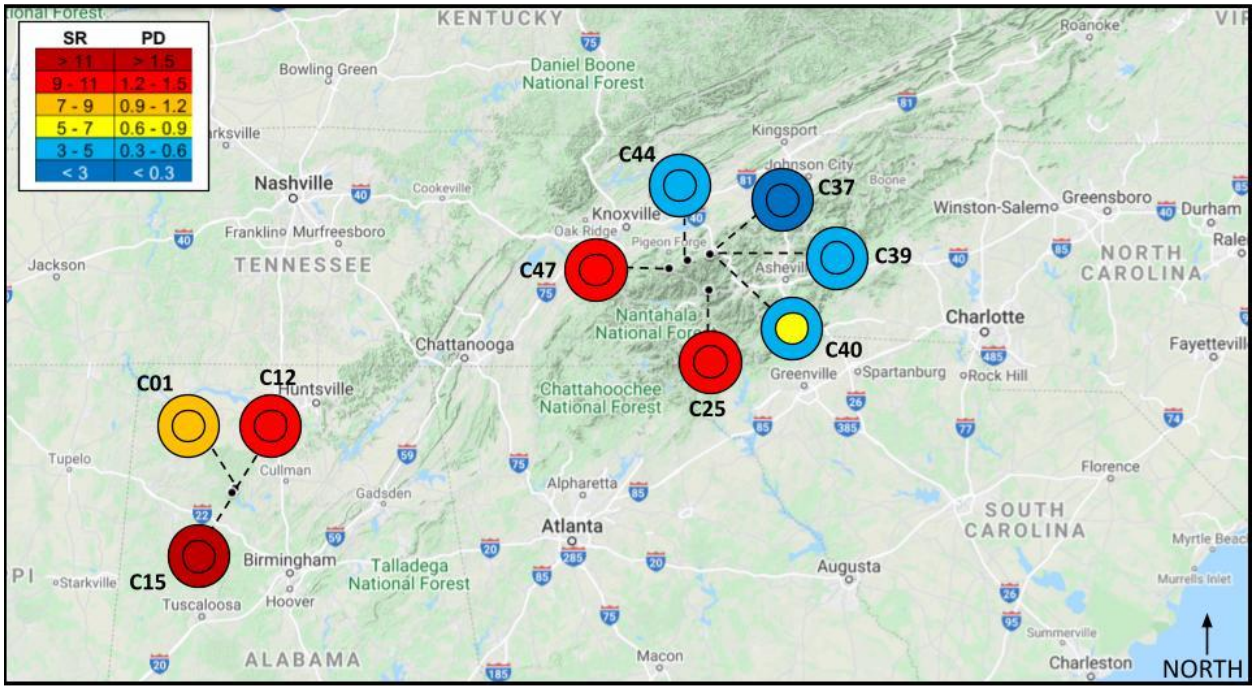

Figure 7: Heat map of centers of biodiversity. Each of nine rotting logs that were sampled are labeled, and represented by a color-coded symbol composed of two circles. The outer circle reflects species richness, and the inner circle reflects phylogenetic diversity. Values of both measures of biodiversity were pooled into six equally sized bins, to simplify color coding. Precise values are shown in Table 6.

DISCUSSION

Unexpectedly higher biodiversity in National Forest, compared to a National Park

Bankhead National Forest had a higher biodiversity and higher species richness in comparison to the Great Smoky Mountains National Park. There are on-going conservation and management efforts in each of the two regions that this study focused on. During the early 2000s, Bankhead National Forest experienced a Southern Pine Beetle (*Dendroctonus frontalis*) infestation at epidemic levels, peaking in the summer of 2000. This beetle species is native to the southern United States, and it can cause mass mortality among pine trees during outbreaks (Havill et al. 2019). In Bankhead National Forest, these attacks began as localized "spots" in areas where trees are stressed (e.g., by drought, or storm damage), but then rapidly expanded to nearby healthy trees. Due to this infestation, the US Forest Service in Alabama developed a Forest Health and Restoration Initiative, which included restoration of six native upland forest community types, including all associated plant and wildlife species (National Resources Leadership Institute 2003). In addition to this plan, commercial logging is common in Bankhead National Forest which, like the occasional pine beetle infestations, creates "pulses" of deadwood inputs on the forest floor. Soon after logging, this deadwood becomes habitable and is therefore

good for invertebrates that depend on this habitat type. However, since all the trees have been logged, there will be a long period without trees falling, resulting in a period of low deadwood habitat availability. Sampling for this study was done relatively soon after the pine beetle infestation and the logging (US Forest Service 2021). This could be a factor that explains the finding of high biodiversity in this forest region.

On the contrary, conservation efforts in the Great Smoky Mountains National Park have focused on preventing impacts of warming climate, since many plants and animals in the park are mountain specialists and found nowhere else. As a member of the Climate Friendly Parks program, Great Smoky Mountains National Park is a part of a nationwide park network that is putting climate-friendly behavior at the forefront of sustainability planning (National Park Service 2021). Since the Great Smoky Mountains National Park is a part of the national park system, the forests are protected from logging, and so they would have a stable inflow deadwood, rather than a "pulse" followed by very few inputs. This contrast with Bankhead National Forest conservation may influence phylogenetic diversity and species richness in their respective rotting log arthropod communities. Although both forest regions are at least partly protected, the different management practices may have had an impact on biodiversity that was detected by this study. However, it remains unknown whether the higher levels of biodiversity in Bankhead National Forest today is going to be short-lived.

Direct comparison of species richness and phylogenetic diversity

Similar to the deadwood associated arthropods in this study, correlation between species richness and phylogenetic diversity is very high for terrestrial bird species across the globe. Areas of low avian phylogenetic diversity occurred at high latitudes and in areas of high relief associated with the Andes and Himalayan mountain ranges. Areas with particularly high phylogenetic diversity were distributed more widely and include islands and isolated regions, such as Australia and Madagascar, as well as ecological transition zones, such as the Sahel and parts of Central America. Drivers of avian phylogenetic diversity include distance to neighboring realms, altitudinal range, and climate stability (Voskamp 2017).

Limitations of this study

Sampling of Bankhead National Forest and Great Smoky Mountains National Park was conducted during the same months of the year, but in different (consecutive) years, and this may have affected results. Also, the difference in species richness and phylogenetic diversity between the two forest regions could be due to differences in the circumference of the logs sampled from each location. Further research including this information could show a correlation between log size and biodiversity. If so, then the size of rotting logs in different forest regions would need to be the same in order for more meaningful comparisons. Rotting log habitats may act similar to

islands for deadwood-associated arthropods. This would mean that the vicinity of other habitable rotting logs might influence colonization, competition, and community diversity. By measuring the number of species per log versus the size of each log versus the vicinity of other logs, a study using theories of insular biogeography could be applied. Finally, there were some unusual groupings in the molecular phylogenetic tree that was used to calculate phylogenetic diversity, indicating that a more accurate tree should be obtained. The ambiguity could've inflated or deflated the measure of phylogenetic diversity to create error; however, it wouldn't affect the results greatly as the measure wouldn't be systematically biased in one direction. More DNA sequence data would help.

Conclusions

Phylogenetic diversity and species richness are useful for identifying communities that require protection. By identifying regions of low and high biodiversity, the information can be used towards assessments of site valuation and prioritization for conservation. This study of deadwood-associated arthropods showed that, unexpectedly, there was higher biodiversity in National Forest than in a National Park. Also, while there was a strong positive correlation between phylogenetic diversity and species richness, phylogenetic diversity provided slightly more information for rank-ordering rotting logs from high to low diversity. Future studies including these two metrics could be applied to other forest regions in the southern Appalachian Mountains, and to other ecological communities to gain a better understanding of how common it is for there to be higher biodiversity in National Forest than in a National Park.

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